



SEQUENCE LISTING

<110> Waldmann, Rainer

<120> MAMMAL NEURONAL ACID SENSING CATIONIC
CHANNEL, CLONING AND APPLICATIONS THEREOF

<130> 989.6701P

<140> 09/129,758

<141> 1998-08-05

<150> PCT/FR98/00270

<151> 1998-02-11

<150> FR 97/01574

<151> 1997-02-11

<150> FR 97/09587

<151> 1997-07-28

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<170> PatentIn Ver. 2.0

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His	Leu	Ala	Asp	Pro	Ser	Val	Leu	Glu	Ala	Leu	Arg	Gln	Lys	Ala	Asn
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Phe	Lys	His	Tyr	Lys	Pro	Lys	Gln	Phe	Ser	Met	Leu	Glu	Phe	Leu	His
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Arg	Val	Gly	His	Asp	Leu	Lys	Asp	Met	Met	Leu	Tyr	Cys	Lys	Phe	Lys
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Thr Arg Tyr Asn Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys Thr	
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Ser Ala Lys Tyr Leu Glu Lys Lys Phe Asn Lys Ser Glu Lys Tyr Ile	
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Ser Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Ala Leu Asn Tyr	
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Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Val Ala Ala Leu Leu Gly	
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Phe Arg Phe Ser Arg Leu Thr Thr Asn Asp Leu Tyr His Ala Gly Glu
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His Tyr Lys Pro Lys Gln Phe Ser Met Leu Glu Phe Leu His Arg Val
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Gly His Asp Leu Lys Asp Met Met Leu Tyr Cys Lys Phe Lys Gly Gln
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Glu Cys Gly His Gln Asp Phe Thr Thr Val Phe Thr Lys Tyr Gly Lys
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Cys Tyr Met Phe Asn Ser Gly Glu Asp Gly Lys Pro Leu Leu Thr Thr
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Gln Asp Glu Tyr Leu Pro Ile Trp Gly Glu Thr Glu Glu Thr Thr Phe
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Ile Gln Gln Asp Glu Tyr Leu Pro Val Trp Gly Glu Thr Asp Glu Thr
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Pro Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly
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cgg att ccc agc cgc gcg tca gct cgc tac ctg gcc cgg aaa tac aac 1200
 Arg Ile Pro Ser Arg Ala Ser Ala Arg Tyr Leu Ala Arg Lys Tyr Asn
 385 390 395 400

cgc agc gag tcc tac att acg gag aat gta ctg gtt ctg gat atc ttc 1248
 Arg Ser Glu Ser Tyr Ile Thr Glu Asn Val Leu Val Leu Asp Ile Phe
 405 410 415

ttt gag gcc ctc aac tat gaa gcg gtg gaa caa aag gcg gcc tat gaa 1296
 Phe Glu Ala Leu Asn Tyr Glu Ala Val Glu Gln Lys Ala Ala Tyr Glu
 420 425 430

gtg tgc gag ctg ctg gga gac att ggg gga cag atg gga ctg ttt att 1344
 Val Ser Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile
 435 440 445

gga gca agc ctg ctt acc atc ctt gag atc ctc gac tat ctc tgt gag 1392
 Gly Ala Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu
 450 455 460

gtt ttc caa gac aga gtc ctg ggg tat ttc tgg aac aga agg agc gct 1440
 Val Phe Gln Asp Arg Val Leu Gly Tyr Phe Trp Asn Arg Arg Ser Ala
 465 470 475 480

caa aag cgc tct ggc aac act ctg ctc cag gaa gag ttg aat ggc cat 1488
 Gln Lys Arg Ser Gly Asn Thr Leu Leu Gln Glu Glu Leu Asn Gly His
 485 490 495

cga aca cat gtt ccc cac ctc agc cta ggg ccc agg cct cct acc act 1536
 Arg Thr His Val Pro His Leu Ser Leu Gly Pro Arg Pro Pro Thr Thr
 500 505 510

ccc tgt gct gtc acc aag aca ctc tct gcc tcc cac cgt acc tgt tac 1584
 Pro Cys Ala Val Thr Lys Thr Leu Ser Ala Ser His Arg Thr Cys Tyr
 515 520 525

ctc gtc aca agg ctc tag 1602
 Leu Val Thr Arg Leu
 530

<210> 10
 <211> 533
 <212> PRT
 <213> rat

<400> 10
 Met Lys Pro Arg Ser Gly Leu Glu Glu Ala Gln Arg Arg Gln Ala Ser
 1 5 10 15
 Asp Ile Arg Val Phe Ala Ser Ser Cys Thr Met His Gly Leu Gly His
 20 25 30

Ile Phe Gly Pro Gly Gly Leu Thr Leu Arg Arg Gly Leu Trp Ala Thr
 35 40 45
 Ala Val Leu Leu Ser Leu Ala Ala Phe Leu Tyr Gln Val Ala Glu Arg
 50 55 60
 Val Arg Tyr Tyr Gly Glu Phe His His Lys Thr Thr Leu Asp Glu Arg
 65 70 75 80
 Glu Ser His Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Ile Asn
 85 90 95
 Pro Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly
 100 105 110
 Thr Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Tyr Leu Arg
 115 120 125
 Ala Leu Gly Gln Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr
 130 135 140
 Phe Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Glu Asp
 145 150 155 160
 Met Leu Leu Asp Cys Arg Tyr Arg Gly Gln Pro Cys Gly Pro Glu Asn
 165 170 175
 Phe Thr Val Ile Phe Thr Arg Met Gly Gln Cys Tyr Thr Phe Asn Ser
 180 185 190
 Gly Ala His Gly Ala Glu Leu Leu Thr Thr Pro Lys Gly Gly Ala Gly
 195 200 205
 Asn Gly Leu Glu Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro
 210 215 220
 Ile Trp Lys Asp Met Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val
 225 230 235 240
 Gln Ile His Ser Gln Asp Glu Pro Pro Ala Ile Asp Gln Leu Gly Phe
 245 250 255
 Gly Ala Ala Pro Gly His Gln Thr Phe Val Ser Cys Gln Gln Gln Gln
 260 265 270
 Leu Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Asn Thr Ala Ser Leu
 275 280 285
 Asp Pro Asp Asp Phe Asp Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro
 290 295 300
 Arg Pro Arg Pro Ser Pro Pro Tyr Ser Leu Ile Gly Cys Arg Leu Ala
 305 310 315 320
 Cys Glu Ser Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Met His
 325 330 335
 Met Pro Gly Asn Ser Pro Val Cys Ser Pro Gln Gln Tyr Lys Asp Cys
 340 345 350

Ala Ser Pro Ala Leu Asp Ala Met Leu Arg Lys Asp Thr Cys Val Cys
 355 360 365

Pro Asn Pro Cys Ala Thr Thr Arg Tyr Ala Lys Glu Leu Ser Met Val
 370 375 380

Arg Ile Pro Ser Arg Ala Ser Ala Arg Tyr Leu Ala Arg Lys Tyr Asn
 385 390 395 400

Arg Ser Glu Ser Tyr Ile Thr Glu Asn Val Leu Val Leu Asp Ile Phe
 405 410 415

Phe Glu Ala Leu Asn Tyr Glu Ala Val Glu Gln Lys Ala Ala Tyr Glu
 420 425 430

Val Ser Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile
 435 440 445

Gly Ala Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu
 450 455 460

Val Phe Gln Asp Arg Val Leu Gly Tyr Phe Trp Asn Arg Arg Ser Ala
 465 470 475 480

Gln Lys Arg Ser Gly Asn Thr Leu Leu Gln Glu Glu Leu Asn Gly His
 485 490 495

Arg Thr His Val Pro His Leu Ser Leu Gly Pro Arg Pro Pro Thr Thr
 500 505 510

Pro Cys Ala Val Thr Lys Thr Leu Ser Ala Ser His Arg Thr Cys Tyr
 515 520 525

Leu Val Thr Arg Leu
 530

<210> 11
 <211> 1948
 <212> DNA
 <213> rat

<220>
 <221> CDS
 <222> (16)..(1704)

<400> 11
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 Me

c cgg ctg ccc gcg acc 51
 a Arg Leu Pro Ala Thr
 10

gcg ctc agc ggc ccg
 Ala Leu Ser Gly Pro G
 15

gc gag cag ccg gcg 99
 rg Glu Gln Pro Ala
 25

ccc gtg gcg gtg gcg gc
 Pro Val Ala Val Ala Ala
 30

ccc gga gga gac ccg agc ggc
 Arg Gln Pro Gly Gly Asp Arg Ser Gly
 35 40

147

gat ccg gcg ctg cag ggg cca ggg gtc gcc cgc agg ggg cgg ccg tcc	195
Asp Pro Ala Leu Gln Gly Pro Gly Val Ala Arg Arg Gly Arg Pro Ser	
45 50 55 60	
ctg agt cgc act aaa ttg cac ggg ctg cgg cac atg tgc gcg ggg cgc	243
Leu Ser Arg Thr Lys Leu His Gly Leu Arg His Met Cys Ala Gly Arg	
65 70 75	
acg gcg gcg gga ggc tct ttc cag cga cgg gcg ctg tgg gtg ctg gcc	291
Thr Ala Ala Gly Gly Ser Phe Gln Arg Arg Ala Leu Trp Val Leu Ala	
80 85 90	
ttc tgc acg tcc ctc ggc ttg ctg ctg tcc tgg tcc tcg aac cgc ctg	339
Phe Cys Thr Ser Leu Gly Leu Leu Leu Ser Trp Ser Ser Asn Arg Leu	
95 100 105	
ctc tac tgg ctc agc ttc ccg tca cac aca cga gtg cac cgt gag tgg	387
Leu Tyr Trp Leu Ser Phe Pro Ser His Thr Arg Val His Arg Glu Trp	
110 115 120	
agc cgc cag ctg ccg ttc ccc gcc gtc acc gtg tgc aac aac aac ccc	435
Ser Arg Gln Leu Pro Phe Pro Ala Val Thr Val Cys Asn Asn Asn Pro	
125 130 135 140	
ctg cgc ttc ccg cgc ctc tcc aag ggg gac ctc tac tac gcg ggc cac	483
Leu Arg Phe Pro Arg Leu Ser Lys Gly Asp Leu Tyr Tyr Ala Gly His	
145 150 155	
tgg cta ggg ctg ctg ctt ccc aac cgc acc gcg cgc ccg ctg gtc agc	531
Trp Leu Gly Leu Leu Leu Pro Asn Arg Thr Ala Arg Pro Leu Val Ser	
160 165 170	
gag ctg ctg cgg ggc gac gag ccg cgc cgc cag tgg ttc cgc aaa ctg	579
Glu Leu Leu Arg Gly Asp Glu Pro Arg Arg Gln Trp Phe Arg Lys Leu	
175 180 185	
gcc gac ttc cgc ctc ttc ctg ccg ccg cgc cac ttc gag ggc atc agc	627
Ala Asp Phe Arg Leu Phe Leu Pro Pro Arg His Phe Glu Gly Ile Ser	
190 195 200	
gct gcc ttc atg gac cgt ttg ggc cac cag ctg gag gat atg ctg ctc	675
Ala Ala Phe Met Asp Arg Leu Gly His Gln Leu Glu Asp Met Leu Leu	
205 210 215 220	
tcc tgc aag tac cgg ggc gag ctc tgt ggc ccg cac aac ttc tcc tca	723
Ser Cys Lys Tyr Arg Gly Glu Leu Cys Gly Pro His Asn Phe Ser Ser	
225 230 235	
gtg ttt aca aaa tac ggg aag tgt tac atg ttt aac tca ggc gag gat	771
Val Phe Thr Lys Tyr Gly Lys Cys Tyr Met Phe Asn Ser Gly Glu Asp	
240 245 250	
ggc aag ccg ctg ctc acc acg gtc aag ggg ggg acg ggc aac ggg ctg	819
Gly Lys Pro Leu Leu Thr Thr Val Lys Gly Gly Thr Gly Asn Gly Leu	
255 260 265	
gag atc atg ctg gac att cag caa gat gag tac ctg ccc atc tgg gga	867
Glu Ile Met Leu Asp Ile Gln Gln Asp Glu Tyr Leu Pro Ile Trp Gly	
270 275 280	

gag aca gag gaa aca acg ttt gaa gca gga gtg aag gtt cag atc cac Glu Thr Glu Glu Thr Thr Phe Glu Ala Gly Val Lys Val Gln Ile His 285 290 295 300	915
agt cag tct gag ccg cct ttc atc caa gag ctg ggc ttt ggg gtg gct Ser Gln Ser Glu Pro Pro Phe Ile Gln Glu Leu Gly Phe Gly Val Ala 305 310 315	963
ccg ggg ttc cag acc ttc gtg gcc aca caa gag cag agg ctc aca tat Pro Gly Phe Gln Thr Phe Val Ala Thr Gln Glu Gln Arg Leu Thr Tyr 320 325 330	1011
ctg ccc cca cca tgg ggg gag tgc cgg tcc tca gag atg gga ctc gac Leu Pro Pro Pro Trp Gly Glu Cys Arg Ser Ser Glu Met Gly Leu Asp 335 340 345	1059
ttc ttt cct gtt tac agc atc aca gcc tgt cgg att gac tgt gag acc Phe Phe Pro Val Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr 350 355 360	1107
cgc tac atc gtg gag aac tgt aac tgc cgc atg gtc cac atg cca ggg Arg Tyr Ile Val Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly 365 370 375 380	1155
gac gcc cct ttc tgc acc cct gag cag cac aag gag tgt gca gag cct Asp Ala Pro Phe Cys Thr Pro Glu Gln His Lys Glu Cys Ala Glu Pro 385 390 395	1203
gcc ctc ggt cta ctg gca gaa aag gac agc aat tac tgt ctc tgc agg Ala Leu Gly Leu Leu Ala Glu Lys Asp Ser Asn Tyr Cys Leu Cys Arg 400 405 410	1251
aca ccc tgc aac ctg aca cgc tac aac aaa gag ctc tcc atg gtg aag Thr Pro Cys Asn Leu Thr Arg Tyr Asn Lys Glu Leu Ser Met Val Lys 415 420 425	1299
atc ccc agc aag acg tca gcc aag tac tta gag aag aaa ttt aac aaa Ile Pro Ser Lys Thr Ser Ala Lys Tyr Leu Glu Lys Lys Phe Asn Lys 430 435 440	1347
tcg gaa aaa tat atc tca gag aac att ctt gtt ctg gac ata ttt ttt Ser Glu Lys Tyr Ile Ser Glu Asn Ile Leu Val Leu Asp Ile Phe Phe 445 450 455 460	1395
gag gcg ctc aat tac gaa aca att gaa cag aag aag gcg tat gaa gtt Glu Ala Leu Asn Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Val 465 470 475	1443
gct gcc tta ctt ggt gac atc ggt ggt cag atg gga ctg ttc att ggt Ala Ala Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly 480 485 490	1491
gct agt ctc ctc aca ata cta gag ctc ttt gat tat att tat gag ctg Ala Ser Leu Leu Thr Ile Leu Glu Leu Phe Asp Tyr Ile Tyr Glu Leu 495 500 505	1539
atc aaa gag aag cta tta gac ctg ctt ggc aaa gaa gaa gag gaa ggg Ile Lys Glu Lys Leu Leu Asp Leu Leu Gly Lys Glu Glu Glu Glu Gly 510 515 520	1587

agc cac gat gag aac atg agc acc tgt gac aca atg cca aac cac tct 1635
 Ser His Asp Glu Asn Met Ser Thr Cys Asp Thr Met Pro Asn His Ser
 525 530 535 540

gaa acc atc agc cac act gtg aac gtg ccc ctg cag aca gct ttg ggc 1683
 Glu Thr Ile Ser His Thr Val Asn Val Pro Leu Gln Thr Ala Leu Gly
 545 550 555

acc ctg gag gag att gcc tgc tgacacctct caggcaacgc agcacctcca 1734
 Thr Leu Glu Glu Ile Ala Cys
 560

aacagacctt aaaggcccaa gacctaggac aggagacagc aagcgcaggt gggatcgccc 1794

ctgacgactg aaagaagcag agccccccat atgcacacat tgcgaacttc tgccaaacct 1854

cacctggcca catctgacat gaaccgtccc gggccctgcg tcatgtccct cgcaggaccg 1914

atgagtcgca ctccggaact gtccaagaac taac 1948

<210> 12

<211> 563

<212> PRT

<213> rat

<400> 12

Met Ser Arg Ser Gly Gly Ala Arg Leu Pro Ala Thr Ala Leu Ser Gly
 1 5 10 15

Pro Gly Arg Phe Arg Met Ala Arg Glu Gln Pro Ala Pro Val Ala Val
 20 25 30

Ala Ala Ala Arg Gln Pro Gly Gly Asp Arg Ser Gly Asp Pro Ala Leu
 35 40 45

Gln Gly Pro Gly Val Ala Arg Arg Gly Arg Pro Ser Leu Ser Arg Thr
 50 55 60

Lys Leu His Gly Leu Arg His Met Cys Ala Gly Arg Thr Ala Ala Gly
 65 70 75 80

Gly Ser Phe Gln Arg Arg Ala Leu Trp Val Leu Ala Phe Cys Thr Ser
 85 90 95

Leu Gly Leu Leu Leu Ser Trp Ser Ser Asn Arg Leu Leu Tyr Trp Leu
 100 105 110

Ser Phe Pro Ser His Thr Arg Val His Arg Glu Trp Ser Arg Gln Leu
 115 120 125

Pro Phe Pro Ala Val Thr Val Cys Asn Asn Asn Pro Leu Arg Phe Pro
 130 135 140

Arg Leu Ser Lys Gly Asp Leu Tyr Tyr Ala Gly His Trp Leu Gly Leu
 145 150 155 160

Leu Leu Pro Asn Arg Thr Ala Arg Pro Leu Val Ser Glu Leu Leu Arg
 165 170 175

Gly Asp Glu Pro Arg Arg Gln Trp Phe Arg Lys Leu Ala Asp Phe Arg
 180 185 190

Leu Phe Leu Pro Pro Arg His Phe Glu Gly Ile Ser Ala Ala Phe Met
 195 200 205

Asp Arg Leu Gly His Gln Leu Glu Asp Met Leu Leu Ser Cys Lys Tyr
 210 215 220

Arg Gly Glu Leu Cys Gly Pro His Asn Phe Ser Ser Val Phe Thr Lys
 225 230 235 240

Tyr Gly Lys Cys Tyr Met Phe Asn Ser Gly Glu Asp Gly Lys Pro Leu
 245 250 255

Leu Thr Thr Val Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu
 260 265 270

Asp Ile Gln Gln Asp Glu Tyr Leu Pro Ile Trp Gly Glu Thr Glu Glu
 275 280 285

Thr Thr Phe Glu Ala Gly Val Lys Val Gln Ile His Ser Gln Ser Glu
 290 295 300

Pro Pro Phe Ile Gln Glu Leu Gly Phe Gly Val Ala Pro Gly Phe Gln
 305 310 315 320

Thr Phe Val Ala Thr Gln Glu Gln Arg Leu Thr Tyr Leu Pro Pro Pro
 325 330 335

Trp Gly Glu Cys Arg Ser Ser Glu Met Gly Leu Asp Phe Phe Pro Val
 340 345 350

Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Ile Val
 355 360 365

Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Phe
 370 375 380

Cys Thr Pro Glu Gln His Lys Glu Cys Ala Glu Pro Ala Leu Gly Leu
 385 390 395 400

Leu Ala Glu Lys Asp Ser Asn Tyr Cys Leu Cys Arg Thr Pro Cys Asn
 405 410 415

Leu Thr Arg Tyr Asn Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys
 420 425 430

Thr Ser Ala Lys Tyr Leu Glu Lys Lys Phe Asn Lys Ser Glu Lys Tyr
 435 440 445

Ile Ser Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Ala Leu Asn
 450 455 460

Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Val Ala Ala Leu Leu
 465 470 475 480

Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Leu Leu
 485 490 495

Thr Ile Leu Glu Leu Phe Asp Tyr Ile Tyr Glu Leu Ile Lys Glu Lys
 500 505 510

Leu Leu Asp Leu Leu Gly Lys Glu Glu Glu Gly Ser His Asp Glu
 515 520 525

Asn Met Ser Thr Cys Asp Thr Met Pro Asn His Ser Glu Thr Ile Ser
 530 535 540

His Thr Val Asn Val Pro Leu Gln Thr Ala Leu Gly Thr Leu Glu Glu
 545 550 555 560

Ile Ala Cys

<210> 13
 <211> 625
 <212> PRT
 <213> Helix aspersa

<400> 13
 Met Lys Tyr Thr Ser Ala Ala Thr Lys Pro Gly Val Phe Pro Glu His
 1 5 10 15

His Gln His Ala Met Met Arg Asn Arg Tyr His Pro His His Cys Asn
 20 25 30

Tyr Ser Asp Asn Arg Ser Ala Ile Asp Ile Ile Ala Glu Leu Gly Ser
 35 40 45

Glu Ser Asn Ala His Gly Leu Ala Lys Ile Val Thr Ser Arg Asp Thr
 50 55 60

Lys Arg Lys Val Ile Trp Ala Leu Leu Val Ile Ala Gly Phe Thr Ala
 65 70 75 80

Ala Thr Leu Gln Leu Ser Leu Leu Val Arg Lys Tyr Leu Gln Phe Gln
 85 90 95

Val Val Glu Leu Ser Glu Ile Lys Asp Ser Met Pro Val Gln Tyr Pro
 100 105 110

Ser Val Ser Ile Cys Asn Ile Glu Pro Ile Ser Leu Arg Thr Ile Arg
 115 120 125

Arg Met Tyr Phe Asn Asn Glu Ser Gln Asn Leu Ile Thr Trp Leu Arg
 130 135 140

Phe Ile Gln Lys Phe Arg Phe Glu Gln Asp Ser Phe Met Asn Ser Ile
 145 150 155 160

Arg Ala Phe Tyr Glu Asn Leu Gly Gln Asp Ala Lys Lys Leu Ser His
 165 170 175

Asn Leu Glu Asp Met Leu Met His Cys Arg Phe Asn Arg Glu Leu Cys
 180 185 190

His Val Ser Asn Phe Ser Thr Phe Phe Asp Gly Asn Tyr Phe Asn Cys
 195 200 205

Phe Thr Phe Asn Ser Gly Gln Arg Leu Gln Met His Ala Thr Gly Pro
 210 215 220

Glu Asn Gly Leu Ser Leu Ile Phe Ser Val Glu Lys Asp Asp Pro Leu
 225 230 235 240

Pro Gly Thr Tyr Gly Val Tyr Asn Phe Asp Asn Asn Ile Leu His Ser
 245 250 255

Ala Gly Val Arg Val Val Val His Ala Pro Gly Ser Met Pro Ser Pro
 260 265 270

Val Asp His Gly Ile Asp Ile Pro Pro Gly Tyr Ser Ser Ser Val Gly
 275 280 285

Leu Lys Ala Ile Leu His Thr Arg Leu Pro Tyr Pro Tyr Gly Asn Cys
 290 295 300

Thr Asn Asp Met Leu Asn Gly Ile Lys Gln Tyr Lys Tyr Thr Phe Phe
 305 310 315 320

Ala Cys Leu Gln Leu Cys Lys Gln Arg Leu Ile Ile Gln Arg Cys Gly
 325 330 335

Cys Lys Ser Ser Ala Leu Pro Glu Val Pro Ser Tyr Asn Ala Thr Phe
 340 345 350

Cys Gly Val Ile Lys Asp Trp Gln Glu Ile Asn Arg Asn His Ser Asn
 355 360 365

Glu Asp His Asn Gln Ser Glu Glu Asp Arg Ala Phe Ile Pro Thr Pro
 370 375 380

Tyr Leu Ala Cys Glu Glu Arg Glu Gln Lys Asn Leu Asn Asn Asp Arg
 385 390 395 400

Thr Tyr Glu Leu Ser Cys Gly Cys Phe Gln Pro Cys Ser Glu Thr Ser
 405 410 415

Tyr Leu Lys Ser Val Ser Leu Ser Tyr Trp Pro Leu Glu Phe Tyr Gln
 420 425 430

Leu Ser Ala Val Glu Arg Phe Phe Lys Gln Glu Arg Gln Ala Gly Gln
 435 440 445

Asn His Phe Met Lys Thr Ala Tyr Glu Tyr Leu Glu Lys Leu Ala His
 450 455 460

Pro Ser Gln Lys His Leu Ala Arg Asn Asp Ser His Met Asp Asp Ile
 465 470 475 480

Leu Ser Lys Ser Tyr Ser Leu Ser Glu Lys Glu Met Ala Lys Glu Ala
 485 490 495

Ser Asp Leu Ile Arg Gln Asn Met Leu Arg Leu Asn Ile Tyr Leu Glu
 500 505 510

Asp Leu Ser Val Val Glu Tyr Arg Gln Leu Pro Ala Tyr Gly Leu Ala
 515 520 525

Asp Leu Phe Ala Asp Ile Gly Gly Thr Leu Gly Leu Trp Met Gly Ile
 530 535 540

Ser Val Leu Thr Ile Met Glu Leu Ile Glu Leu Val Ile Arg Leu Thr
 545 550 555 560

Gly Leu Val Phe Asn Ser Glu Lys Gly Leu Pro Arg Gly Pro Thr Thr
 565 570 575

Val Asn Asn Asn Asn Gly Ser Asn Asn His Ser Gln Ser Thr Ser Gln
 580 585 590

His Gln Leu Tyr Asn Gly Tyr Met Asp His Asp Ser His Tyr Ser Asp
 595 600 605

Ser Ala Gly Ala Ser Val Phe Asp Phe Arg Arg Gly Val Glu Ser Pro
 610 615 620

Val
 625

<210> 14
 <211> 564
 <212> PRT
 <213> C. elegans

<220>
 <221> SITE
 <222> (180)
 <223> Xaa represents 207 non-disclosed amino acids

<400> 14
 Met Ser Trp Met Gln Asn Leu Lys Asn Tyr Gln His Leu Arg Asp Pro
 1 5 10 15

Ser Glu Tyr Met Ser Gln Val Tyr Gly Asp Pro Leu Ala Tyr Leu Gln
 20 25 30

Glu Asn Thr Lys Phe Val Thr Glu Arg Glu Tyr Tyr Glu Asp Phe Gly
 35 40 45

Tyr Gly Glu Cys Phe Asn Ser Ser Glu Ser Glu Val Gln Cys Glu Leu
 50 55 60

Ile Thr Gly Glu Phe Asp Pro Lys Leu Leu Pro Tyr Asp Lys Arg Leu
 65 70 75 80

Ala Trp His Phe Lys Glu Phe Cys Tyr Lys Thr Ser Ala His Gly Ile
 85 90 95

Pro Met Ile Gly Glu Ala Pro Asn Val Tyr Tyr Arg Ala Val Trp Val
 100 105 110

Met Leu Phe Leu Gly Cys Met Ile Met Leu Tyr Leu Asn Ala Gln Ser
 115 120 125

Val Leu Asp Lys Tyr Asn Arg Asn Glu Lys Ile Val Asp Ile Gln Leu
 130 135 140

Phe Lys Phe Asp Thr Ala Pro Phe Pro Ala Ile Thr Leu Cys Asn Leu
 145 150 155 160
 Asn Pro Tyr Lys Ala Ser Leu Ala Thr Ser Val Asp Leu Val Lys Arg
 165 170 175
 Thr Leu Ser Xaa Glu Ile Trp Thr Tyr Leu Gln Gly Gly Thr Pro Thr
 180 185 190
 Glu Asp Pro Asn Phe Leu Glu Ala Met Gly Phe Gln Gly Met Thr Asp
 195 200 205
 Glu Val Ala Ile Val Thr Lys Ala Lys Glu Asn Ile Met Phe Ala Met
 210 215 220
 Ala Thr Leu Ser Met Gln Asp Arg Glu Arg Leu Ser Thr Thr Lys Arg
 225 230 235 240
 Glu Leu Val His Lys Cys Ser Phe Asn Gly Lys Ala Cys Asp Ile Glu
 245 250 255
 Ala Asp Phe Leu Thr His Ile Asp Pro Val Phe Gly Ser Cys Phe Thr
 260 265 270
 Phe Asn His Asn Arg Thr Val Asn Leu Thr Ser Ile Arg Ala Gly Pro
 275 280 285
 Met Tyr Gly Leu Arg Met Leu Val Tyr Val Asn Ala Ser Asp Tyr Met
 290 295 300
 Pro Thr Thr Glu Ala Thr Gly Val Arg Leu Thr Ile His Asp Lys Glu
 305 310 315 320
 Asp Phe Pro Phe Pro Asp Thr Phe Gly Tyr Ser Ala Pro Thr Gly Tyr
 325 330 335
 Val Ser Ser Phe Gly Leu Arg Leu Arg Lys Met Ser Arg Leu Pro Ala
 340 345 350
 Pro Tyr Gly Asp Cys Val Pro Asp Gly Lys Thr Ser Asp Tyr Ile Tyr
 355 360 365
 Ser Asn Tyr Glu Tyr Ser Val Glu Gly Cys Tyr Arg Ser Cys Phe Gln
 370 375 380
 Gln Leu Val Leu Lys Glu Cys Arg Cys Gly Asp Pro Arg Phe Pro Val
 385 390 395 400
 Pro Glu Gly Ala Arg His Cys Asp Ala Ala Asp Pro Val Ala Arg Arg
 405 410 415
 Cys Leu Asp Ala Arg Met Asn Asp Leu Gly Gly Leu His Gly Ser Phe
 420 425 430
 Arg Cys Arg Cys Gln Gln Pro Cys Gly Gln Ser Ile Tyr Ser Val Thr
 435 440 445
 Tyr Ser Pro Ala Lys Trp Pro Ser Leu Ser Leu Gln Ile Gln Leu Gly
 450 455 460

Ser Cys Asn Gly Thr Ala Val Glu Cys Asn Lys His Tyr Lys Glu Asn
 465 470 475 480

Gly Ala Met Val Glu Val Phe Tyr Glu Gln Leu Asn Phe Glu Met Leu
 485 490 495

Thr Glu Ser Glu Ala Tyr Gly Phe Val Asn Leu Leu Ala Asp Phe Gly
 500 505 510

Gly Gln Leu Gly Leu Trp Cys Gly Ile Ser Phe Leu Thr Cys Cys Glu
 515 520 525

Phe Val Phe Leu Phe Leu Glu Thr Ala Tyr Met Ser Ala Glu His Asn
 530 535 540

Tyr Ser Leu Tyr Lys Lys Lys Lys Ala Glu Lys Ala Lys Lys Val Ala
 545 550 555 560

Ser Gly Ser Phe

<210> 15
 <211> 24
 <212> DNA
 <213> degenerate primer

<220>
 <221> modified_base
 <222> (various positions)
 <223> "n" at positions 6, 9, 12, 15 & 16 represents
 "inosine", while "n" at position 18 represents A,
 T, C, G or unknown

<400> 15
 ttyccngcncr tnacnntntg yaay

24

<210> 16
 <211> 26
 <212> DNA
 <213> degenerate primer

<220>
 <221> modified_base
 <222> (various positions)
 <223> "n" at positions 3, 6, 9, 11 & 12 represents
 "inosine", while "n" at positions 15 & 18 represents A,
 T, C, G or unknown

<400> 16
 canarnccna nntgnccncc dawrtc

26

<210> 17
 <211> 20
 <212> DNA
 <213> primer

<400> 17
 attgctcttc ccatctctat

20

<210> 18
<211> 20
<212> DNA
<213> primer

<400> 18
ttcaaggccc atacctaagt

20